On May 24, 2005, more than 50 people participated in a one day workshop on the "Use of the Rabbit to Model Infectious Diseases of Humans." The meeting was organized by the NIAID and DMID and therefore, represented the infectious disease segment of the rabbit community. One of the purposes of the workshop was to present established rabbit models of infectious diseases including bacterial (*Treponema pallidum, Mycobacterium tuberculosis,* enterohemorrhagic *E. coli),* fungal (*Candida, Aspergillus sp., Coccidioides immitis),* and viral (papillomavirus) pathogens. In addition, several select agents of bioterrorism (*Bacillus anthracis, Francisella tularensis)* and a rabbit orthologue (rabbit poxvirus) were also considered. The gamut of research presented ranged from bacterial pathogenesis, disease models, vaccine development, oncologic complications, and immunotherapy. In the context of agents of bioterrorism, the implications of the FDA "Animal Rule" were also outlined for the participants.

A state-of-the-art series of lectures on the immunogenetics of the rabbit summarized B-cell sequence diversification as well as mucosal immunology in the rabbit as it compared to human. Harnessing the well-known ability of rabbits to produce large amounts of high avidity antibody to specific antigens, the use of the rabbit for generation of humanized therapeutic monoclonal and fully human polyclonal antibodies for therapy of human diseases was also outlined.

An update from the Broad Institute was presented to the participants on the now completed 2x rabbit genome sequence. Scaffolds of the sequence compared well with other mammalian genomes that have been covered at higher density. The contiguity of the low coverage sequence, however, is problematic for recovering genes of interest in their full genomic context. Analysis of the number of genes that can be found within the 2x sequence and the proportion of the entire gene sequence that can be recovered is on-going using a web browser that compares reference sequences from the complete human genome to that of the rabbit.

Finally, there was a discussion of the practical considerations associated with working with rabbits and rabbit cells and tissues. Researchers who have assembled immunologic and reagent resources for the swine community spoke of their experience in centralizing resources. In addition to the recognized need for more complete genome sequence coverage, a list of priorities that would have the greatest positive impact on research with rabbits was compiled. A centralized web-based resource for all who use rabbits in research was proposed to post successfully used reagents, protocols, primer sequences, as well as development of a principal investigators list serve.